

FIGURE 1A

9.1 (SEQ ID NO:1): 5' GGGAGAGAGG AAGAGGGAUG GG CCGCCAGU
GGGAAGCUAU ACCCAACGCC CCAGCCCCAG AGCAUAACCC AGAGGUCGAU AGUACUGGAU
CCCCC 3'

9.2 (SEQ ID NO:2): 5' GGGAGAGAGG AAGAGGGAUG GGCUAUAUAC ACGCUGGUGA
UCCCAUCUCA AUUGAAACAA CACUAACCC AGAGGUCGAU AGUACUGGAU CCCCC 3'

9.3 (SEQ ID NO:3): 5' GGGAGAGAGG AAGAGGGAUG GGGACUAUAC CGCGUAAUGC
UGCCUCCCCA UCCCGGAACG CUCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCC 3'

9.4 (SEQ ID NO:4): 5' GGGAGAGAGG AAGAGGGAUG GGCACUAUAC GCAUCUUGCU
GCCUGCCCGC GAGUCAAAU GCAUAACCCA GAGGUCGAU GUACUGGAUC CCCCC 3'

9.5 (SEQ ID NO:5): 5' GGGAGAGAGG AAGAGGGAUG GGCCUACCAG UUCGUGGCUA
GCGUGACGUA CCACCCAGG ACCUAACCC AGAGGUCGAU AGUACUGGAU CCCCC 3'

9.7 (SEQ ID NO:6): 5' GGGAGAGAGG AAGAGGGAUG GGCGAUAACC AACAUUGUGA
UCCCAUUC AUACCCUAC AACUAACCC AGAGGUCGAU AGUACUGGAU CCCCC 3'

9.8 (SEQ ID NO:7): 5' GGGAGAGAGG AAGAGGGAUG GGGCCACCUA CUAUACCGGU
CAUCGUGCAU AGGUCGCUGC CACUAACCC AGAGGUCGAU AGUACUGGAU CCCCC 3'

9.9 (SEQ ID NO:8): 5' GGGAGAGAGG AAGAGGGAUG GGUCUCACAC CCGAAGAUGG
CCAAAGAGGG AGAUGAGUUU CCAUAACCCA GAGGUCGAU GUACUGGAUC CCCCC 3'

9.11 (SEQ ID NO:9): 5' GGGAGAGAGG AAGAGGGAUG GGACUAUAUU CGGAUUCUGG
ACUCCCACCU GCCUGCCCCA GACUAACCC AGAGGUCGAU AGUACUGGAU CCCCC 3'

9.12 (SEQ ID NO:10): 5' GGGAGAGAGG AAGAGGGAUG GGCGAUAUAC
ACAUUGGUGA UCCCACCCAC AUGAAACCAC AGCAUAACCC AGAGGUCGAU AGUACUGGAU
CCCCC 3'

9.13 (SEQ ID NO:11): 5' GGGAGAGAGG AAGAGGGAUG GGCUCAUCAC
AGGCGAAGUG AACACACUA CCGNCNAGUU ACCUAACCC AGAGGUCGAU AGUACUGGAU
CCCCC 3'

9.14 (SEQ ID NO:12): 5' GGGAGAGAGG AAGAGGGAUG GG GACUAUAC
GUGAACGACU GCAUCCACUUC CCcGCCAUGG CAUAACCCAG AGGUCGAUAG
UACUGGAUCC CCCC 3'

FIGURE 1B

9.16 (SEQ ID NO:13): 5' GGGAGAGAGG AAGAGGGAUG GGCCAUACGU
GGACGACUGC ACCCGACCCU UCAGCCCAGG UCCAUAACCC AGAGGUCGAU AGUACUGGAU
CCCCC 3'

9.17 (SEQ ID NO:14): 5' GGGAGAGAGG AAGAGGGAUG GGACCAUACG
CACAUUGCUG AAUCCCCcUC AAUAGCACCU ACCAUAAACCC AGAGGUCGAU AGUACUGGAU
CCCCC 3'

9.18 (SEQ ID NO:15): 5' GGGAGAGAGG AAGAGGGAUG GGCCAUAAAC
ACUUUGGUGA ACCCACCAG CUCc/UUGUGAU UGCAUAACCC AGAGGUCGAU
AGUACUGGAU CCCCC 3'

9.19 (SEQ ID NO:16): 5' GGGAGAGAGG AAGAGGGAUG GGACCAUAAC
GACUACUCGUGA AUCCACCAU CAGCGCACAA CAUAACCCAGA GGUCGAUAG
UACUGGAUCC CCCC 3'

9.20 (SEQ ID NO:17): 5' GGGAGAGAGG AAGAGGGAUG GGGACUAUAC
CGGCAUUCGU GCAUCCCCUG GACCUAACAA UACUAACCC AGAGGUCGAU AGUACUGGAU
CCCCC 3'

9.21 (SEQ ID NO:18): 5' GGGAGAGAGG AAGAGGGAUG GG AACACCAU
UAAUGCUCGG CCAGGUAACC CCGGCGCAUA CUCAUAACCC AGAGGUCGAU AGUACUGGAU
CCCCC 3'

9.25 (SEQ ID NO:19): 5' GGGAGAGAGG AAGAGGGAUG GGGACCAUAA
CUCUAACGGG UGAAUCCCCG AUCUCGACAA UACUAACCC AGAGGUCGAU AGUACUGGAU
CCCCC 3'

9.26 (SEQ ID NO:20): 5' GGGAGAGAGG AAGAGGGAUG GG UGAUAACC
ACUCUGGUGA ACCCCUCCCG ACUUGCUCGC ACAUAACCCA GAGGUCGAUA GUACUGGAUC
CCCC 3'

9.27 (SEQ ID NO:21): 5' GGGAGAGAGG AAGAGGGAUG GGUAUAUACU
GUAUGGUGAA CCCACCCAAA CUCCCAUGGC UACUAACCC AGAGGUCGAU AGUACUGGAU
CCCCC 3'

9.28 (SEQ ID NO:22): 5' GGGAGAGAGG AAGAGGGAUG GG CGCCAUAC
GCACAUUGC U GCAUCGCCU CCCGUAAGAA CCAUAACCCA GAGGUCGAUA GUACUGGAUC
CCCC 3'

10560-23560

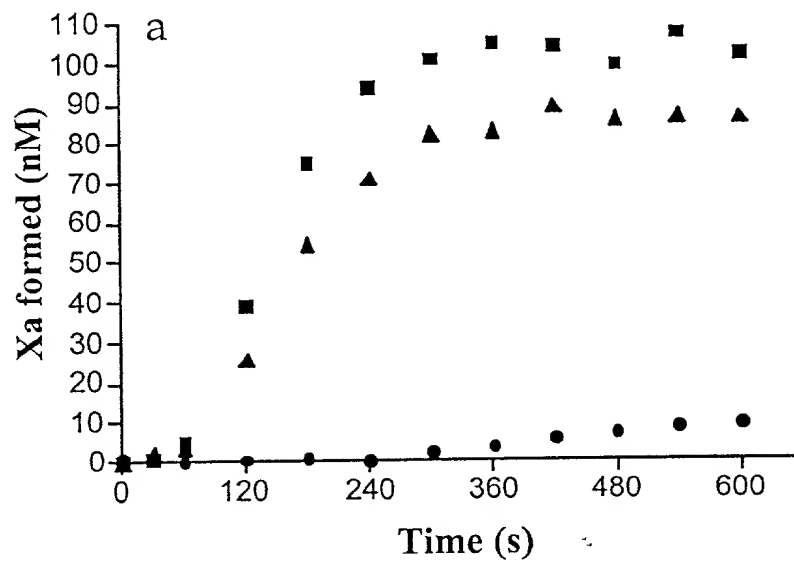
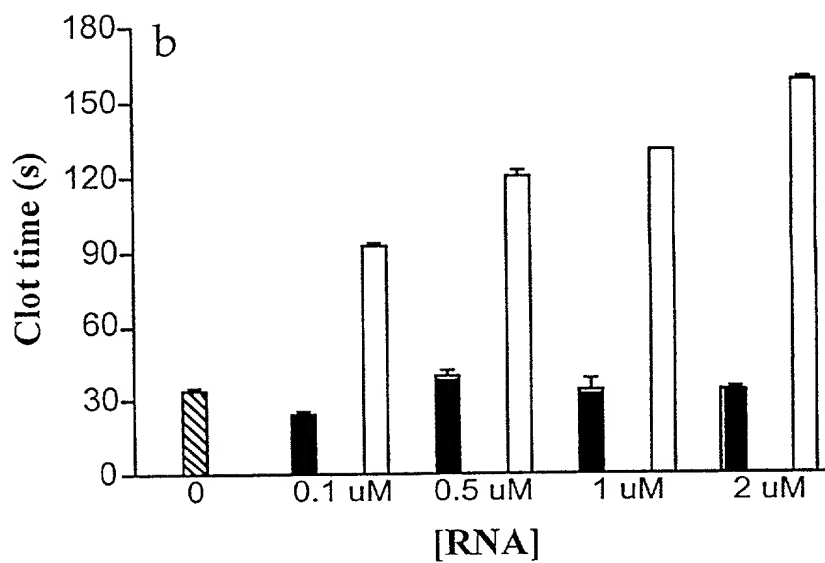


FIGURE 2A

FIGURE 2B



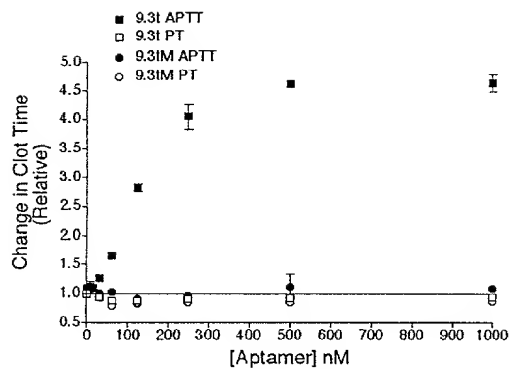


Figure 3A

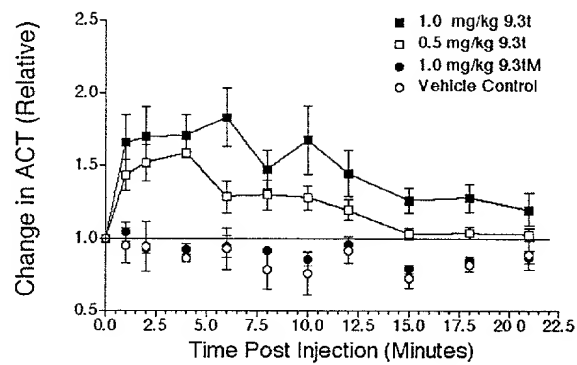


Figure 3B

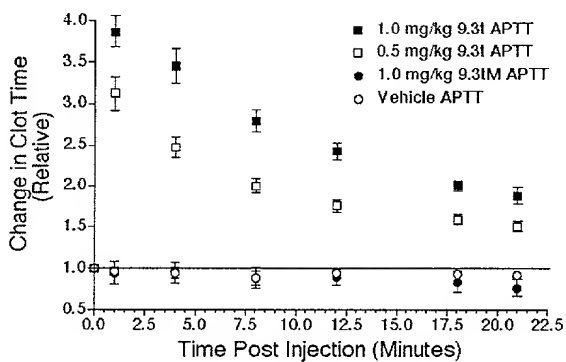


Figure 3C

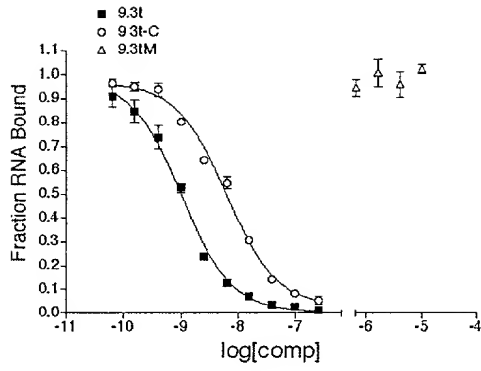


Figure 4A

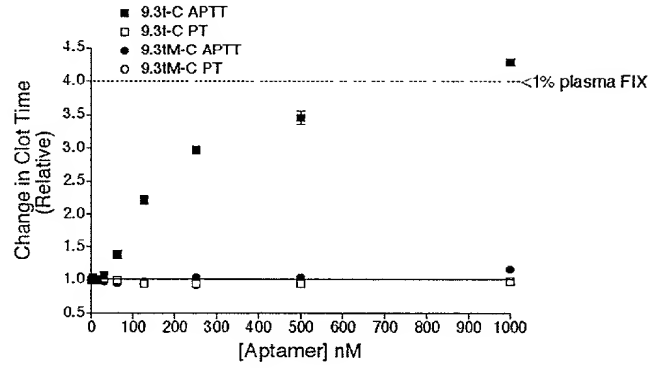


Figure 4B

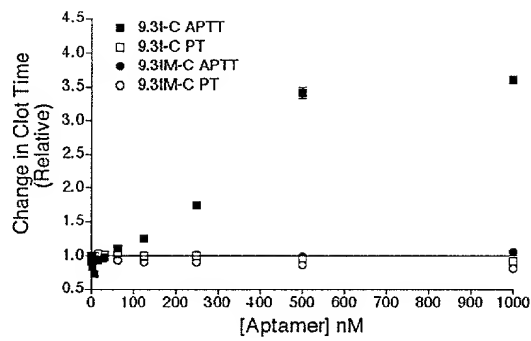


Figure 4C

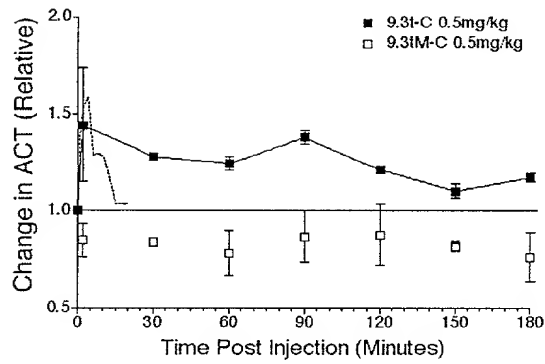


Figure 5A

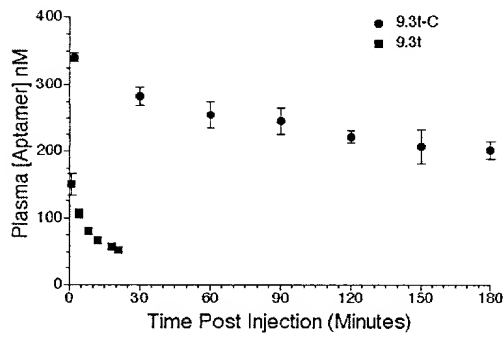


Figure 5B

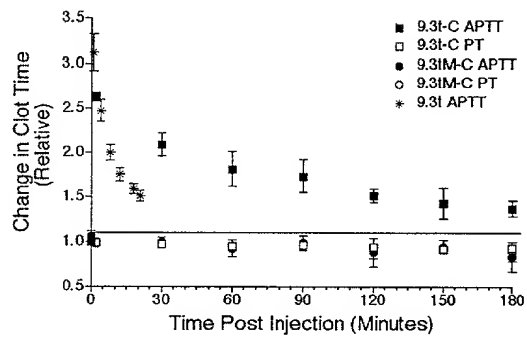


Figure 5C

Figure 6A

10.1 (SEQ ID NO:23): 5' GGGAGAGAGG AAGAGGGAUG GGAAAAUAGC
CCCAGCGAGA UAAUACUUGG CCCCCGUACCA CCAUAACCCA GAGGUCGAUA
GUACUGGAUC CCCC 3'

10.5 (SEQ ID NO:24): 5' GGGAGAGAGG AAGAGGGAUG GGCCAGAAGG
AACUAAACAC CUGAACCCCC CAUCGCGAGAG ACCAUAACCC AGAGGUCGAU
AGUACUGGAU CCCCC 3'

10.6 (SEQ ID NO:25): 5' GGGAGAGAGG AAGAGGGAUG GGAUGUCACU
UGGCCCCUCG CGCACc/acGCC AGCGAGCCCC UAACCCAGAG GUCGAUAGUA
CUGGAUCCCC CC 3'

10.7 (SEQ ID NO:26): 5' GGGAGAGAGG AAGAGGGAUG GGACACGCCC
AGCGAGCUCA AACUUGGCCC CCGUGCAUCA CC CCAUAACC CAGAGGUCGA
UAGUACUGGA UCCCCC 3'

10.8 (SEQ ID NO:27): 5' GGGAGAGAGG AAGAGGGAUG GGAAGUGCCA
CAGCGAGCAC AUGACUUGG CCGCAUUGC ACCCAUAACC CAGAGGUCGA UAGUACUGGA
UCCCCC 3'

10.11 (SEQ ID NO:28): 5' GGGAGAGAGG AAGAGGGAUG GGAAACUAAU
GCCCUAGCGA GCAUACCCGG ACUGGCCCCG CCAUAACCC AGAGGUCGAU AGUACUGGAU
CCCCC 3'

10.12 (SEQ ID NO:29): 5' GGGAGAGAGG AAGAGGGAUG GGAAAAUAGC
CCCAGCGAGA UAAUACUUGG CCCCUCUACU ACCCAUAACC CAGAGGUCGA UAGUACUGGA
UCCCCC 3'

10.13 (SEQ ID NO:30): 5' GGGAGAGAGG AAGAGGGAUG GGCGACCCCA
CUGGCGGAAA CCGACAAUCA CUCCCCACGA CCAUAACCC AGAGGUCGAU AGUACUGGAU
CCCCC 3'

10.14 (SEQ ID NO:73): 5' GGGAGAGAGG AAGAGGGAUG GGAAAAUAGC
CCCAGCGAGA UAAUACUUGG CCCCUCUACU ACCCAUAACC AGAGGUCGAU AGUACUGGAU
CC 3'

Figure 6B

10.15 (SEQ ID NO:31): 5' GGGAGAGAGG AAGAGGGAUG GGCAGCCCAG
CGAGGGACAC UUAACCCCCU GUCCCCAUC CAAACCAUAA CCCAGAGGUC GAUAGUACUG
GAUCCCCC 3'

10.18 (SEQ ID NO:32): 5' GGGAGAGAGG AAGAGGGAUG GGCCAGAAGU
CACCGCGACG GUACUGAACC CCCACCCAA ACCCAUAACC CAGAGGUCGA UAGUACUGGA
UCCCCC 3'

10.19 (SEQ ID NO:33): 5' GGGAGAGAGG AAGAGGGAUG GGCCAGAAGU
GCUCACUACA ACGCUUUGAC CCCCCCAUCC ACAUCCCAUA ACCCAGAGGU CGAUAGUACU
GGAUCCCCC 3'

10.21 (SEQ ID NO:34): 5' GGGAGAGAGG AAGAGGGAUG GG CCAGCAAC
CGAAGGGCGG AAUACCCCCC GUCUCCACAU ACCCAUAACC CAGAGGUCGA UAGUACUGGA
UCCCCC 3'

10.22 (SEQ ID NO:35): 5' GGGAGAGAGG AAGAGGGAUG GG ACGCGACU
CAGGCAGCAC UUGACUUGGC CCCUUGCGAU CACCAUAACC CAGAGGUCGA UAGUACUGGA
UCCCCC 3'

10.23 (SEQ ID NO:36): 5' GGGAGAGAGG AAGAGGGAUG GG CCAGCAAC
GCUAACACGG AAUACCCCCC ACCCAACGU GCCCAUAACC CAGAGGUCGA UAGUACUGGA
UCCCCC 3'

10.24 (SEQ ID NO:37): 5' GGGAGAGAGG AAGAGGGAUG GG CUUCUCAA
CCGAAAUACA ACUUUAAAUC AUUUAUCACU UACCAUAACC CAGAGGUCGA UAGUACUGGA
UCCCCC 3'

10.30 (SEQ ID NO:38): 5' GGGAGAGAGG AAGAGGGAUG GGAUACGCCG
AUGCAAGCAU GUCCACACAC CGCAUGCCGU ACCCAUAACC CAGAGGUCGA UAGUACUGGA
UCCCCC 3'

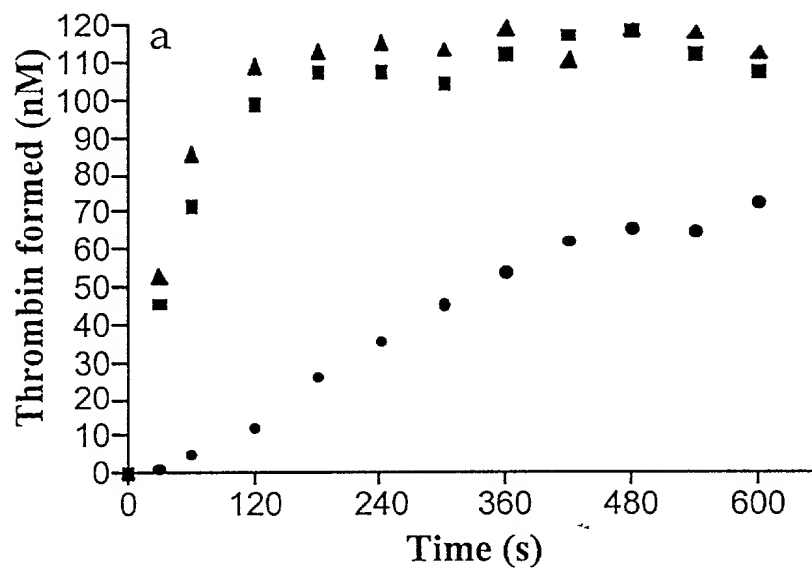
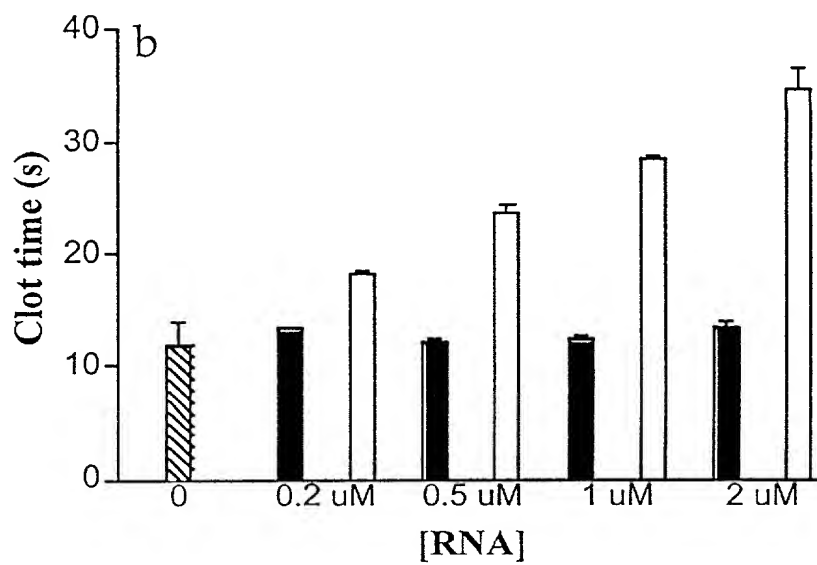


Figure 7A

Figure 7B



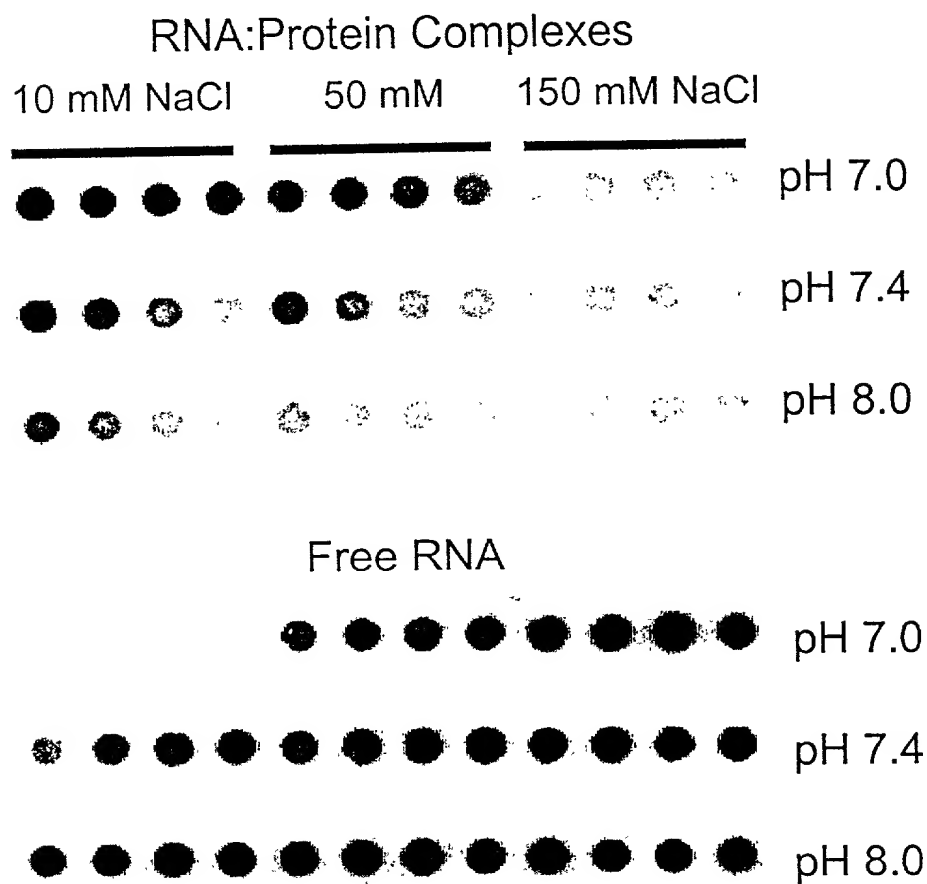
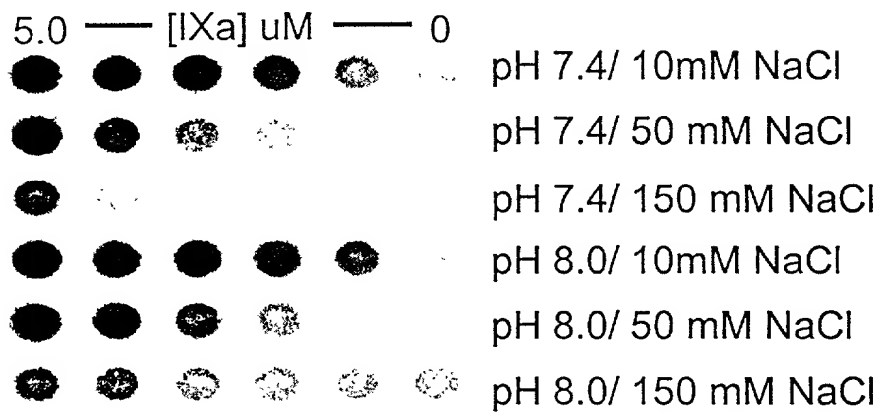


FIGURE 8

RNA:Protein Complexes



Free RNA

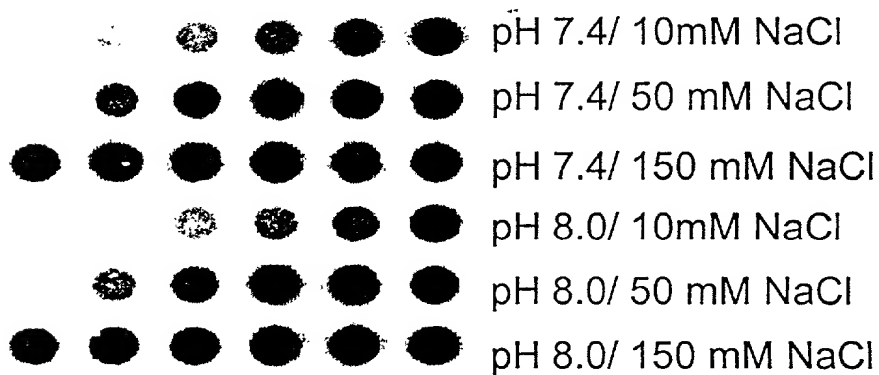


FIGURE 9

Figure 10

16.1: (SEQ ID NO:39) 5' GGGAGAGAGG AAGAGGGAUG GGUACAGAGG AGUACAAGUA
GCAUGGUCCC CUCGUGUAAA AACAUAAACC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.2 (SEQ ID NO:40): 5' GGGAGAGAGG AAGAGGGAUG GGUGCAAAAG AGCUUCUUGU
AGUAUGAUCC CUCAACCGCA AGCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.3 (SEQ ID NO:41): 5' GGGAGAGAGG AAGAGGGAUG GG UACAGAGG AGUACAAGUA
GCAUGAUCCC CUCGUGUAAA AACAUAAACC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.5 (SEQ ID NO:42): 5' GGGAGAGAGG AAGAGGGAUG GGAGCCUAUG UAACAGAUGC
AGAUGCCUAG UCGUCCCAAC ACCAUAAACC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.7 (SEQ ID NO:43): 5' GGGAGAGAGG AAGAGGGAUG GGCACAACGA ACACCGCAUC
CCUUGACAGA AAGAGCACGC CUCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.10 (SEQ ID NO:44): 5' GGGAGAGAGG AAGAGGGAUG GGUACAGAGG AGUACAAGUA
ACAUGAUCCC CUCGUGUAAA AACAUAAACC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.11 (SEQ ID NO:45): 5' GGGAGAGAGG AAGAGGGAUG GG CACAACGA ACACCGCAUC
CCUUGACAGA AAGAACACGC CUCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.18 (SEQ ID NO:46): 5' GGGAGAGAGG AAGAGGGAUG GGCACAAGGA ACACCGCAUC
CCUUGACAGA AAGAACACGC CUCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

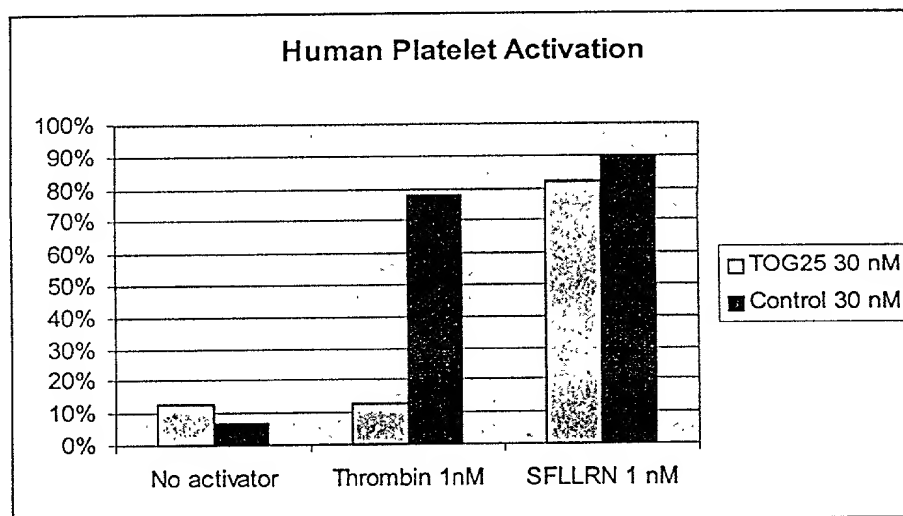
16.20 (SEQ ID NO:47): 5' GGGAGAGAGG AAGAGGGAUG GGAGCCUAUG UAACAGAUGC
AGAUGCCUAG ACGACCCAAC ACCAUAAACC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

180/124/2-23960

FIGURE 11

Random region sequences (Round 13)	K _d Human Thrombin	K _d Porcine Thrombin
FIG 5 UGCGAACAAAGCUGAAGUACUUACGCACAACCCGUAGAAU	3 nM	1 nM
FIG 7 AACAAACUGAAGAACUACCCUUCUACUGACGAAUUA	1 nM	<0.5 nM
FIG 8 AAACAAAGCUGAAGUACUUAUCCAUCACCACGCCGAA	1 nM	0.5 nM
FIG 10 UAUUUGGCUUCUCAGUGCCGCAGAGACAGCAACAAUUAGU	>>50 nM	0.5 nM
HUMAN ACAAAGCUGGAGAACUUACCGUCCUCUCCAGAGAUCAA	2 nM	0.5 nM
TOGGLE 25 GAACAAAGCUGAAGUACUUACCCAAGAUAUCCCGAACGA	5 nM	0.5 nM
TOGGLE 30 AACAAAGCUGGAGAACUUAACGUCCUCUCCAGCGGUAA	3 nM	0.5 nM

FIGURE 12



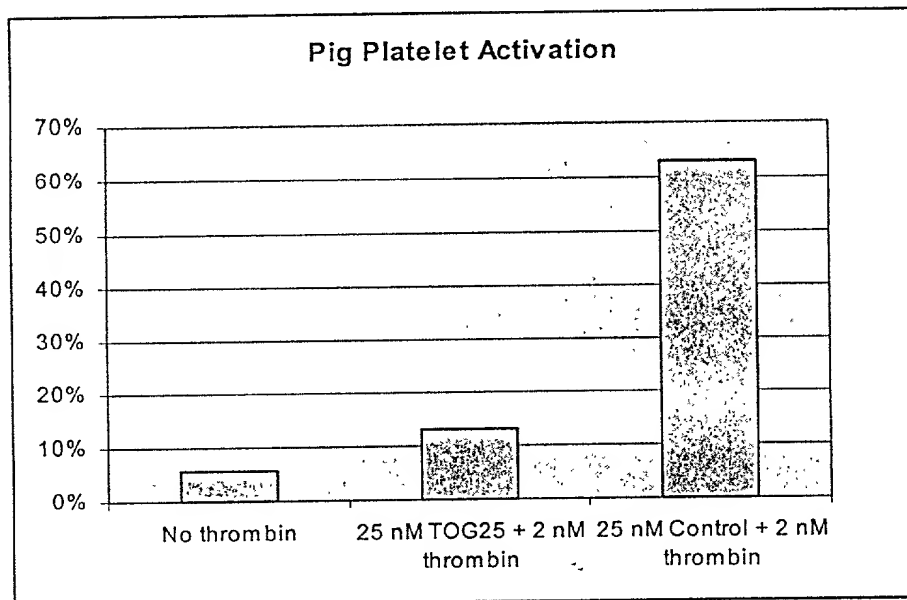


FIGURE 13

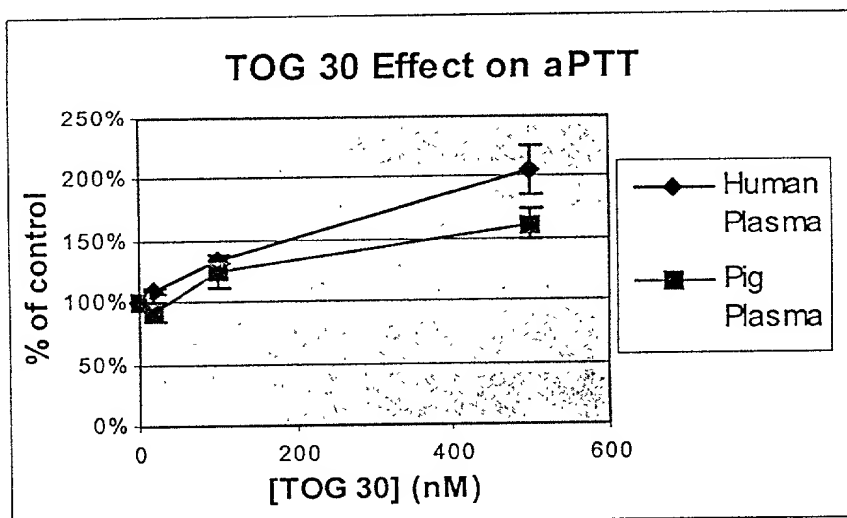


FIGURE 14

Figure 15

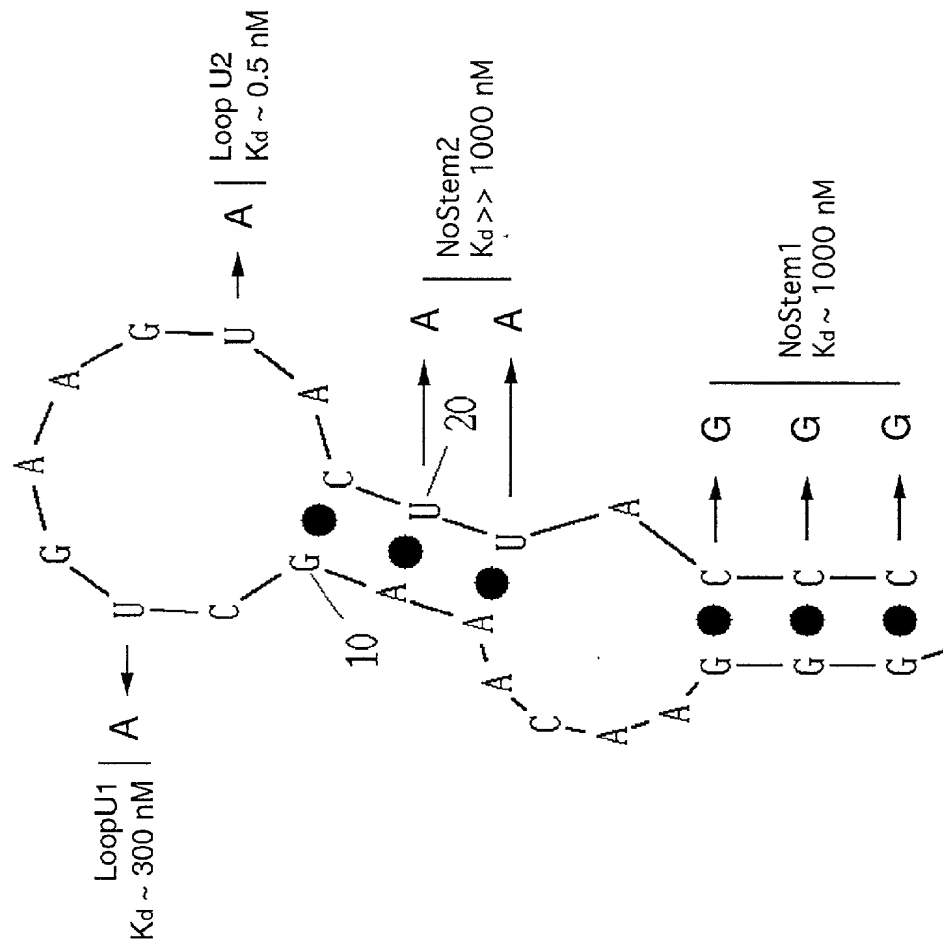


Figure 16

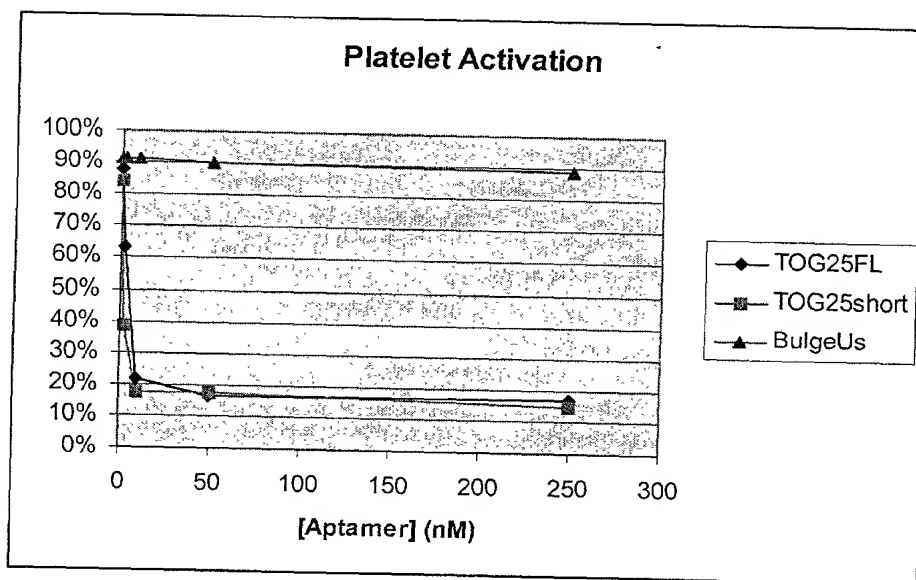


Figure 17

E2F-3 Round 10 Aptamers

5' Primer GGG AGA GAG GAA GAG GGA UGG G (SEQ ID NO: 62)

3' Primer C AUA ACC CAG AGG UCG A A GUA CUG GAUCCC CCC (SEQ ID NO: 63)

10-1 and 10-8 (SEQ ID NO: 64)

5' P-AAUGGA AUC ACUGAA GGC CCUCCG UAG CAC CUA ACA CAGU-3' P

10-2 (SEQ ID NO: 65)

5' P-GCAUCC UGC CAG CGG CGA CGG ACC UGC GCC CAC AGG CCUC-3' P

10-3, 10-7, 10-11, and 10-12 (SEQ ID NO: 66)

5' P-UUA UA AGC ACA CUG AAG CCC UCA GCA AAA CCUCCA CAG G-3' P

10-4 (SEQ ID NO: 67)

5' P-UAU GAA AUC ACA GAA GCC CGC GUU CGA CAC CUC CAC UGUU 3' P

10-5 (SEQ ID NO: 68)

5' P-CAA ACUCAC AGA CUC CAA CUG CAG GAG CAC CCA CCC ACA CUG
GGA CAG-3' P

10-6 (SEQ ID NO: 69)

5' P-AUC CCC GCC GUA AGC CGUCCUGAUGGA CAC CAC ACUCCG C-3' P

1036937-0000-0000-0000-0000-0000

	S1	L1	S2	L2	S2	L3	S1
	→		→		←		←
*9-3 5'	gggaugggGA	CUAUACC	GCG	UAAUGC	UGC	C	UCCCCAUUCC
*9-20 5'	augggGA	CUAUACCG	GCA	AUCG	UGC	A	UCCCCU
*9-25 5'	gggaugggGA	CCAUUA	ACUC	UAAU	GGGU	GAA	UCCCGCAUCU
*9-26 5'	gggauggg	UGAUA	ACCA	CUC	UGGU	GAA	CCCCUCCC
*9-28 5'	gggaugggCG	CCAUAC	GCA	CAU	UGC	UGCAU	CGCCUUCCC
*9-19 5'	gaggggaugggA	CCAUUA	ACGA	CUAC	UCGU	GAA	UCCCACCAUC
9-17 5'	gaggggaugggA	CCAUAC	GCA	CAU	UGC	UGAA	UCCCCCUC
9-11 5'	gggaugggA	CUAUA	UUCGG	AAU	CUGGA		CUCCCACCU
9-4 5'	gggaugggCA	CUAUAC	GCA	UCU	UGC		UGCCUGCCC
9-16 5'	aggggauggg	CCAUUA	CGU	GG	ACG	ACUGCA	CCCGACCCU
9-18 5'	gggauggg	CCAUUA	ACCA	CUU	UGGU	GAA	CCCACCCA
9-7 5'	ggauggg	CGAUA	ACCA	ACA	UGGU	GAU	CCCAUUC
9-12 5'	gggauggg	CGAUA	UAC	ACAUG	GUG	AU	CCCACCC
9-2 5'	gggauggg	CUAUUA	CAC	GCUG	GUG	AU	CCCAUCUC
9-14 5'	gggaugggGA	CUAUA	CGU	GAACG	ACU	GCA	UCCACUCCCC
9-27 5'	gggauggg	UAAUA	ACU	GUA	UGG	UGAA	CCCACCC

FIGURE 18

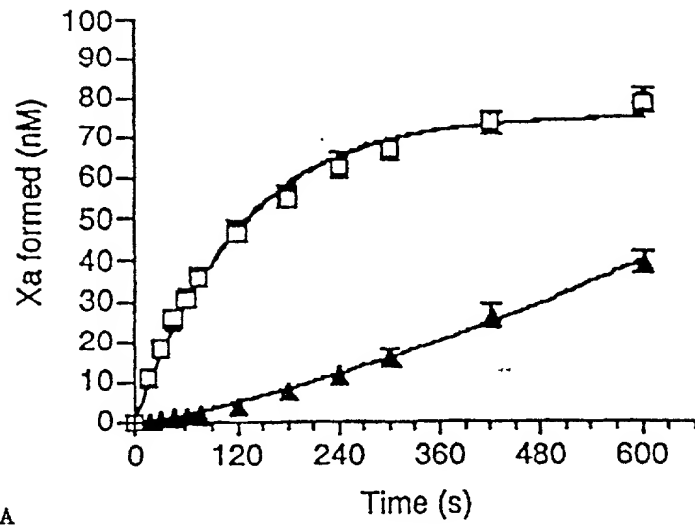


Fig. 19A

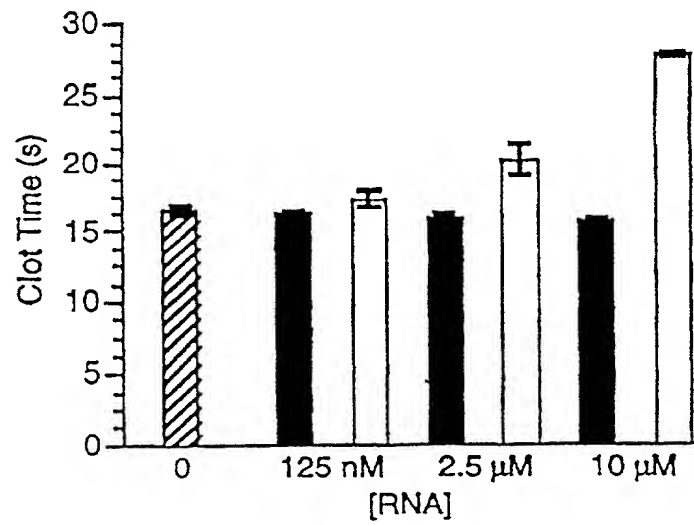
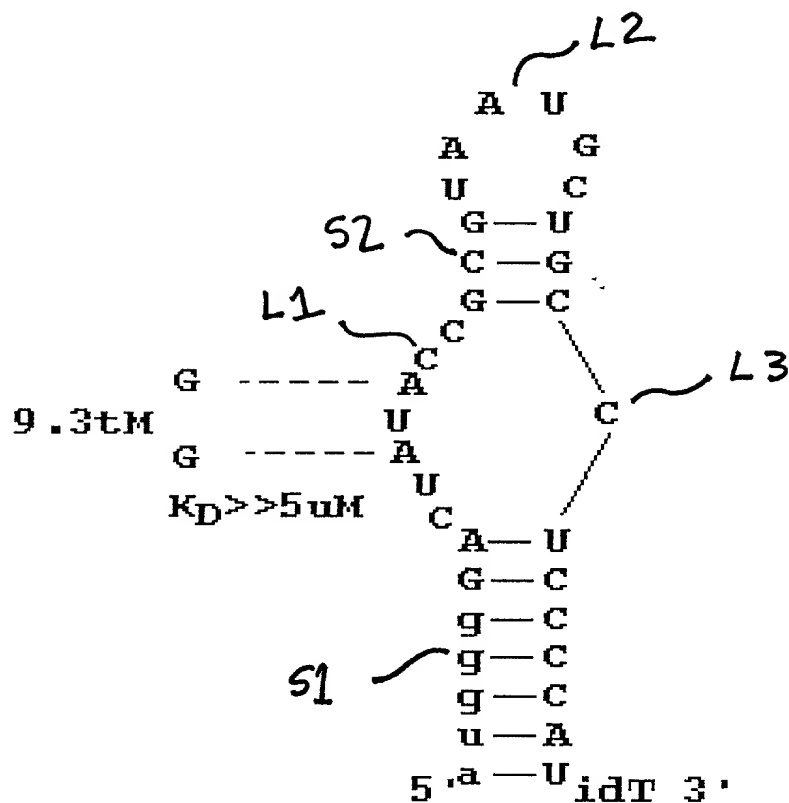


Fig. 19B

Figure 20



109660-2889660

U A A U
 A G C A
 A U
 G U
 C G
 G C C C
 C C C C
 C G C
 G C
 A U
 G C
 A U
 G U
 5' 3'

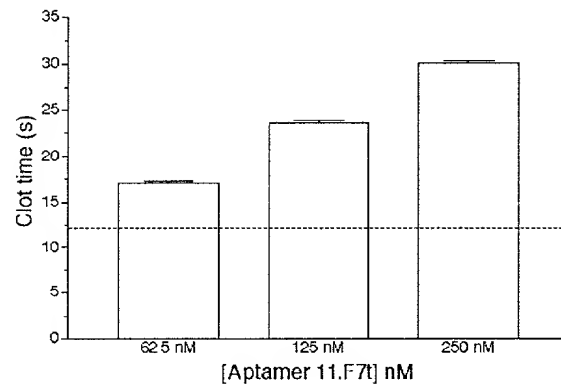


Figure 22A

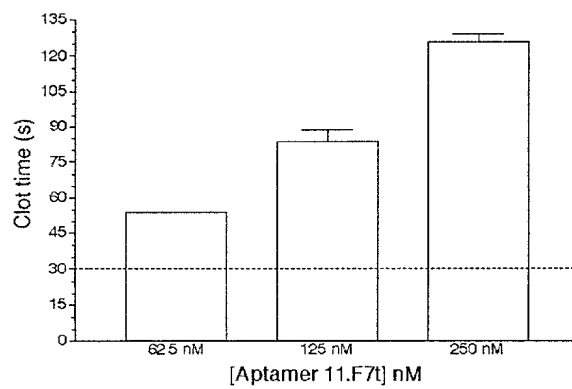


Figure 22B

Figure 23A

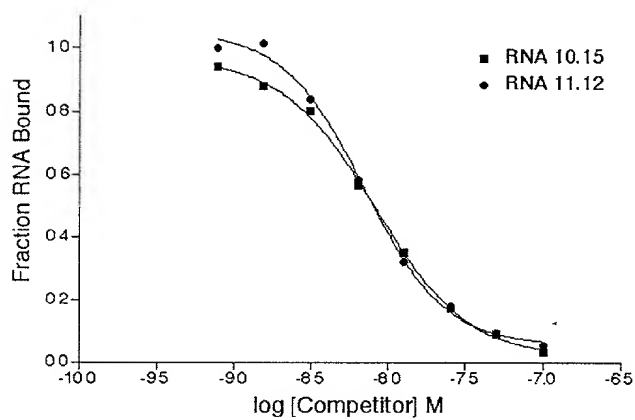


Figure 23B

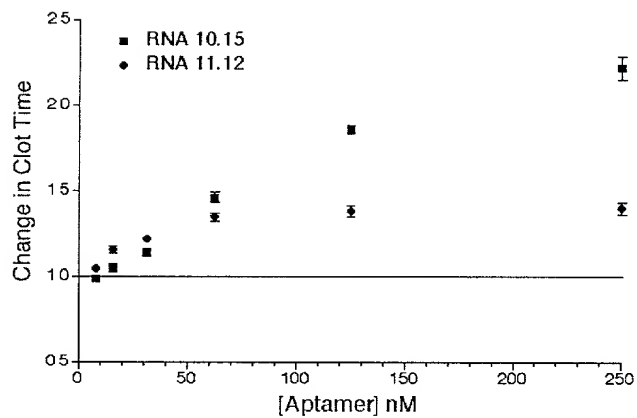


Figure 24

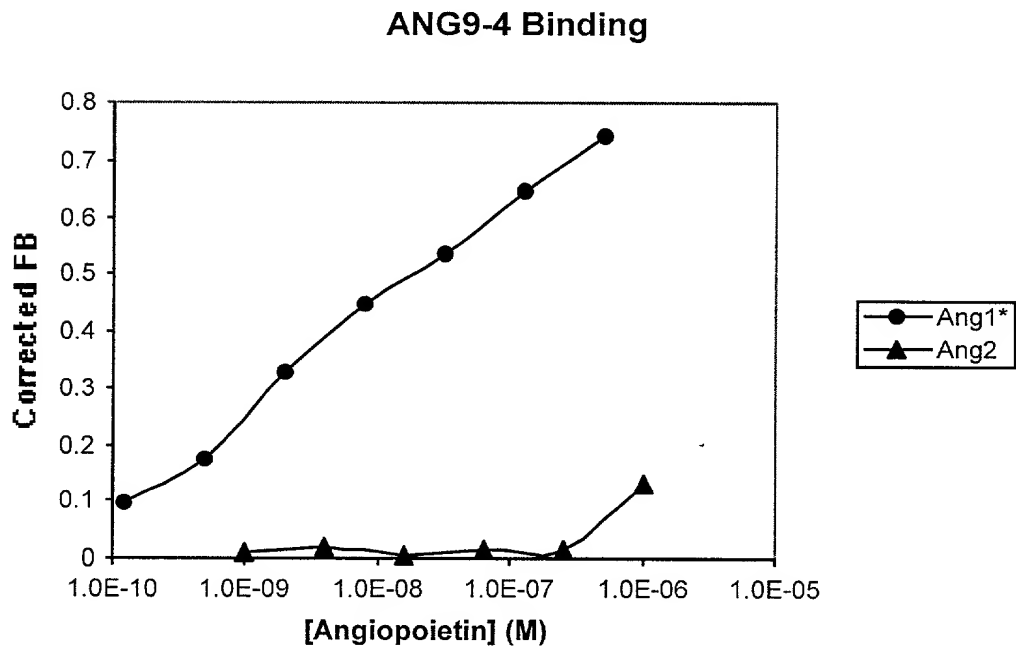
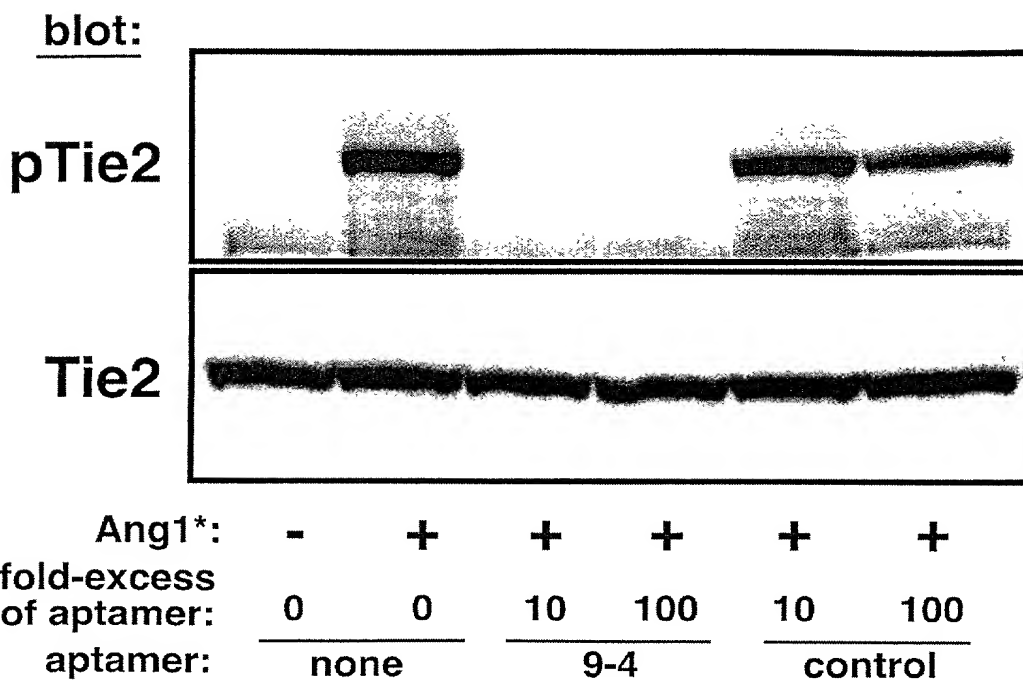
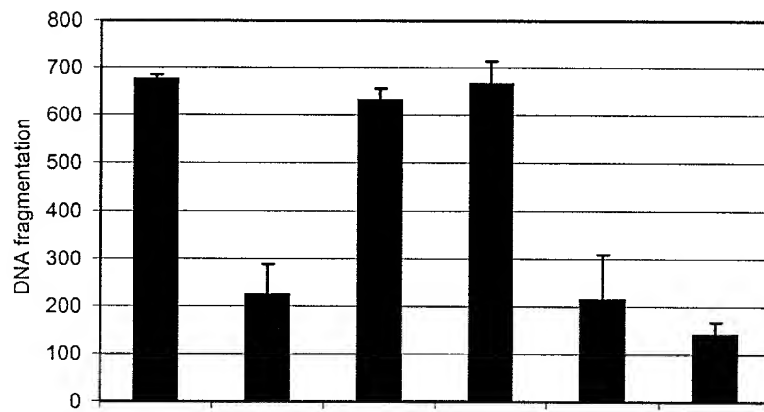


Figure 25





Angl:	-	+	+	+	+	+
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Aptamer:	none		9-4		control	

Figure 26

ANG11-1 Binding

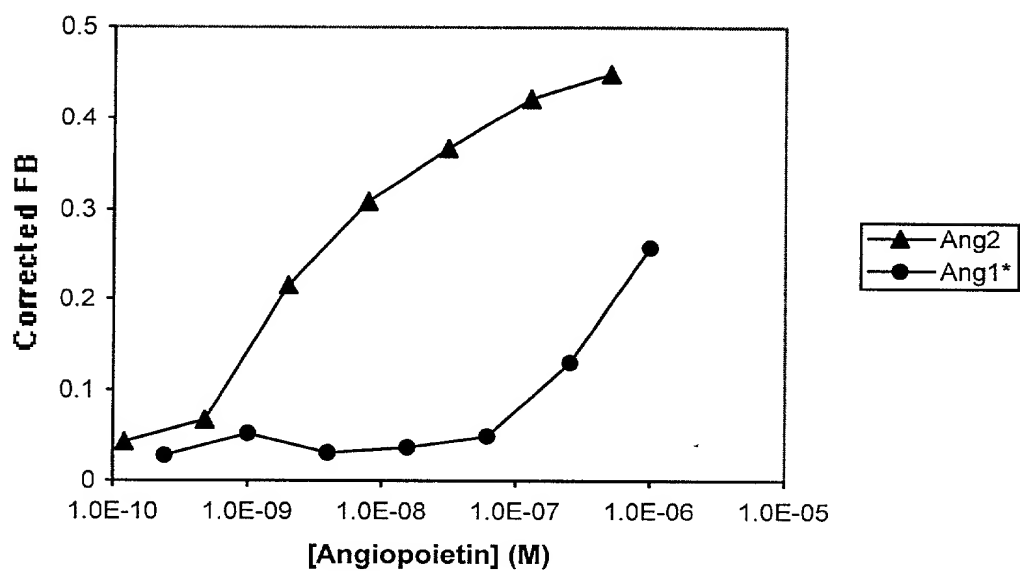
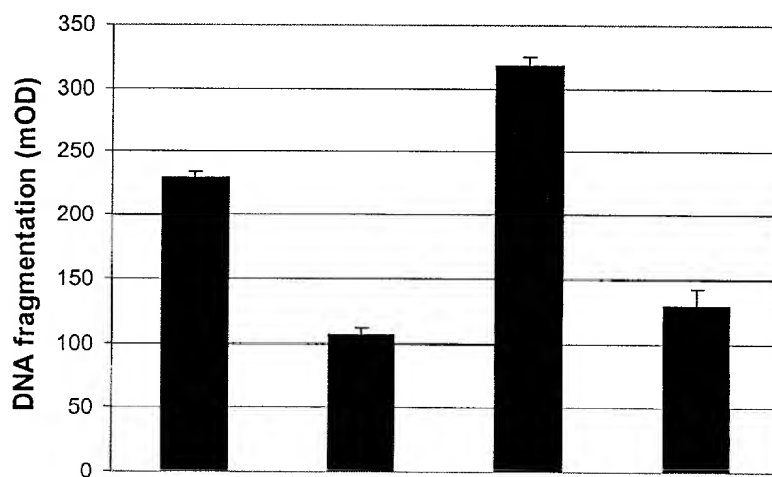


Figure 27



Ang2:

Fold-excess aptamer:

Aptamer:

-	+	+	+
0	0	10	10
none		11-1	control

Figure 28

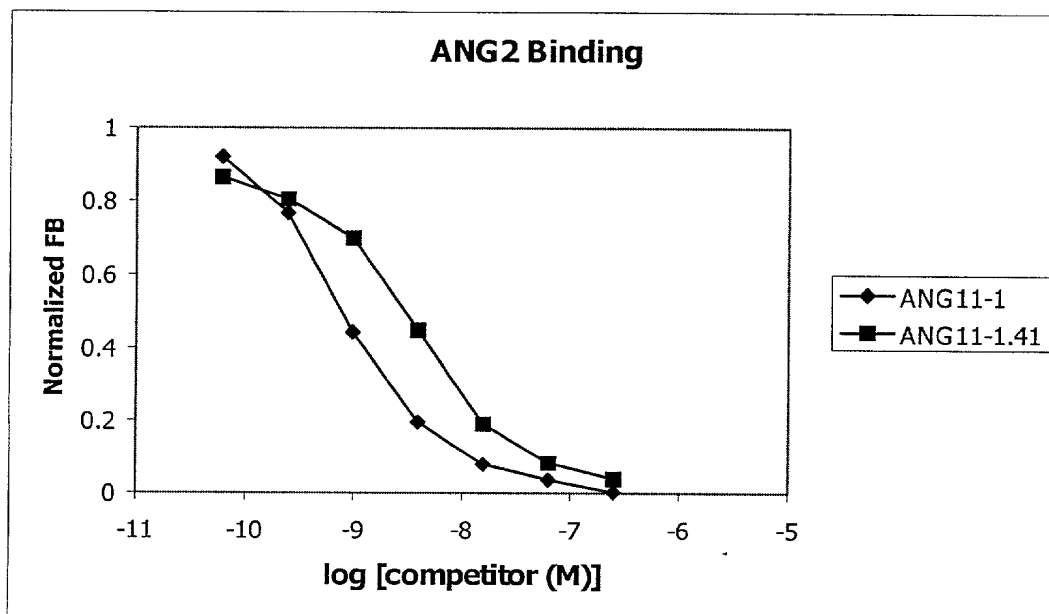
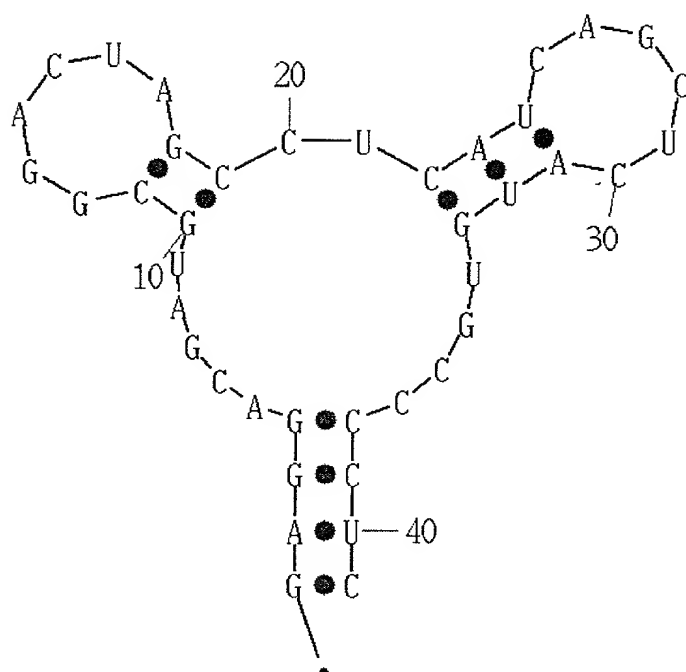


Figure 29

10960-233500

p1422.jpg by D. Stewart and M. Zuker
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$dG = -1.43$ [initially -4.2] ANG11-1.41

Figure 30

Figure 31

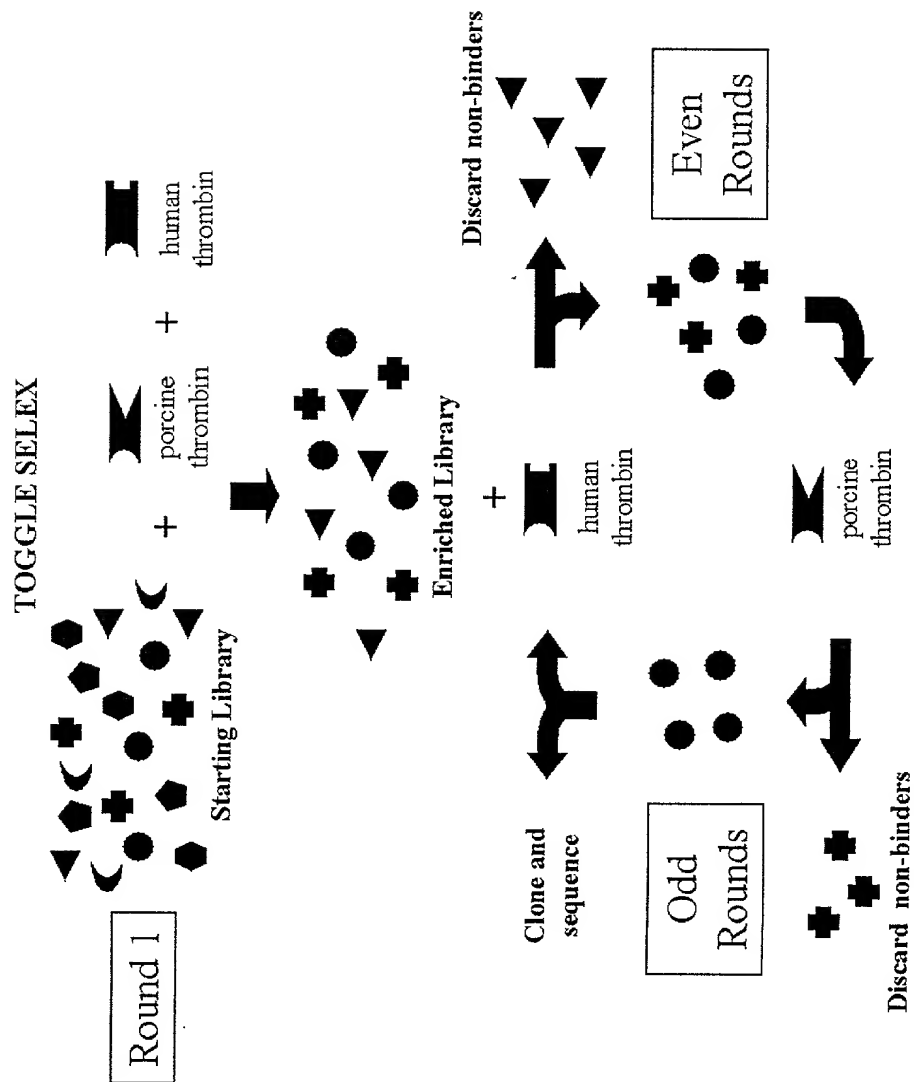


Figure 32

